Report

Summary



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- Per sequence quality scores
- Per base sequence content
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- Overrepresented sequences
- Adapter Content

Basic Statistics

Measure Value

Filename bad_sequence.txt

File type Conventional base calls

Encoding Illumina 1.5

Total Sequences 395288

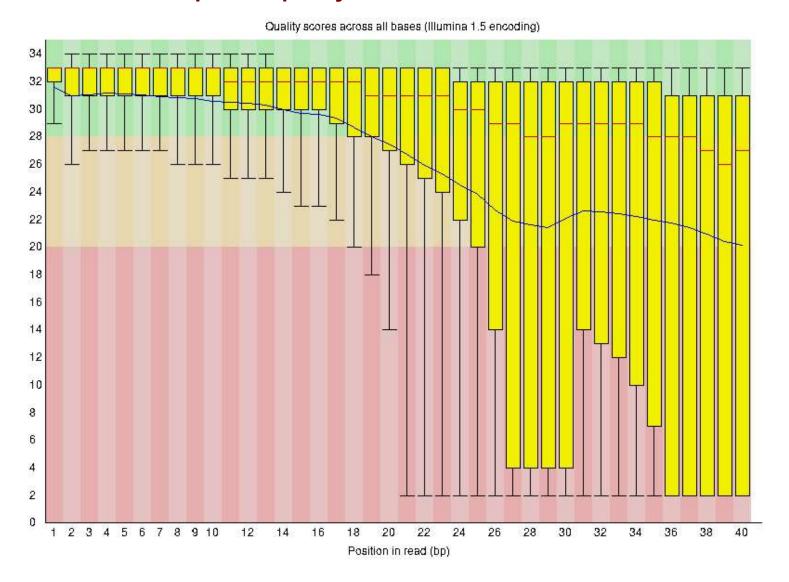
Total Bases 15.8 Mbp

Sequences flagged as poor quality $\,$ 0 $\,$

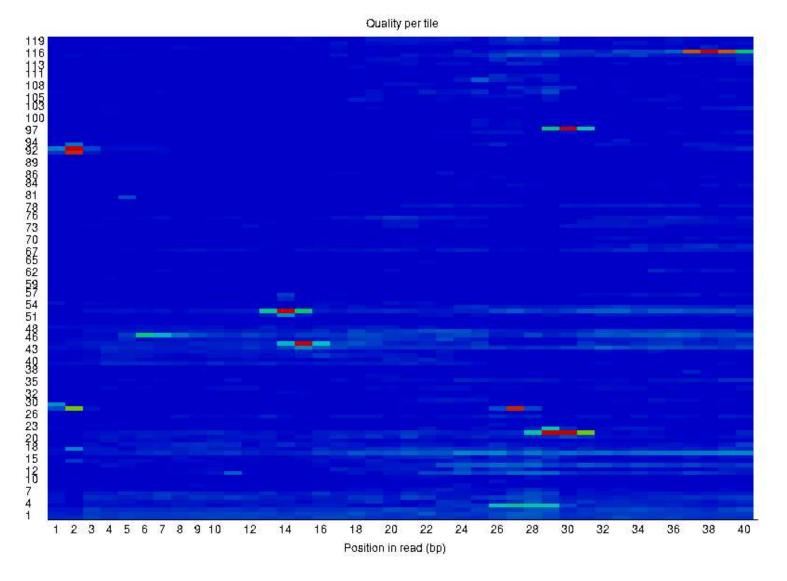
Sequence length 40

%GC 47

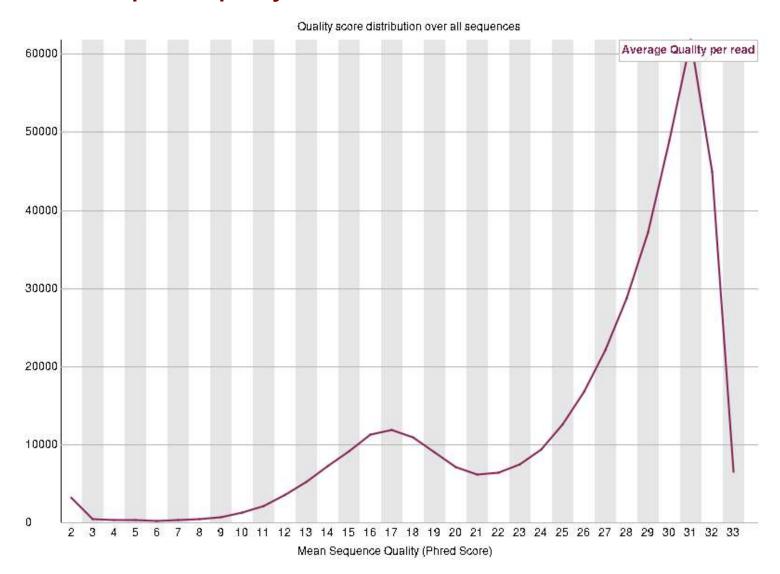
Per base sequence quality



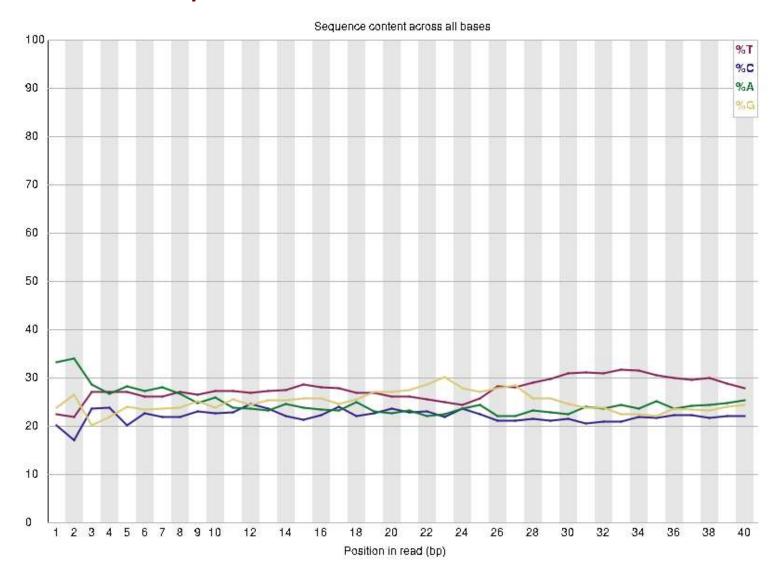
②Per tile sequence quality



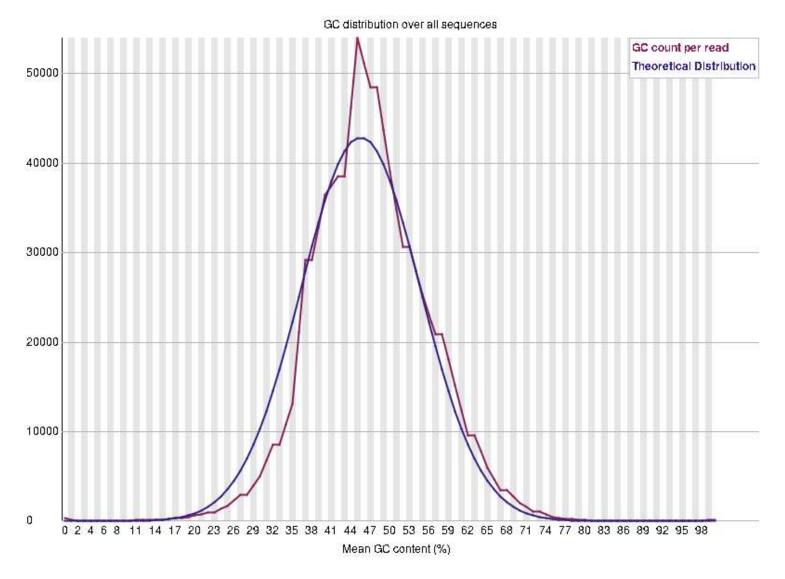
Per sequence quality scores



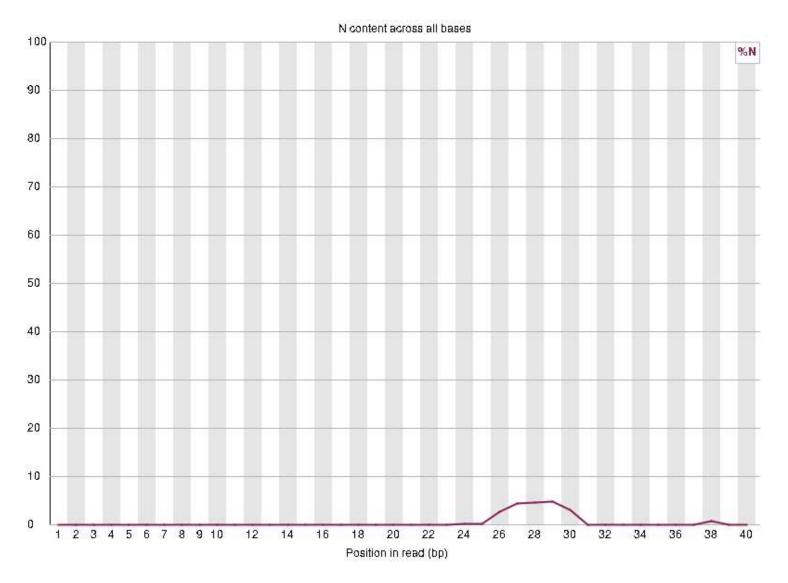
Per base sequence content



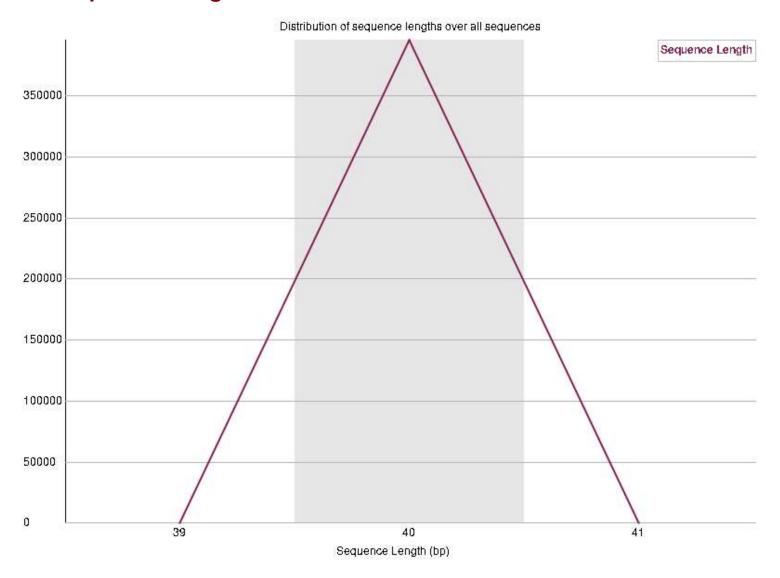
Per sequence GC content



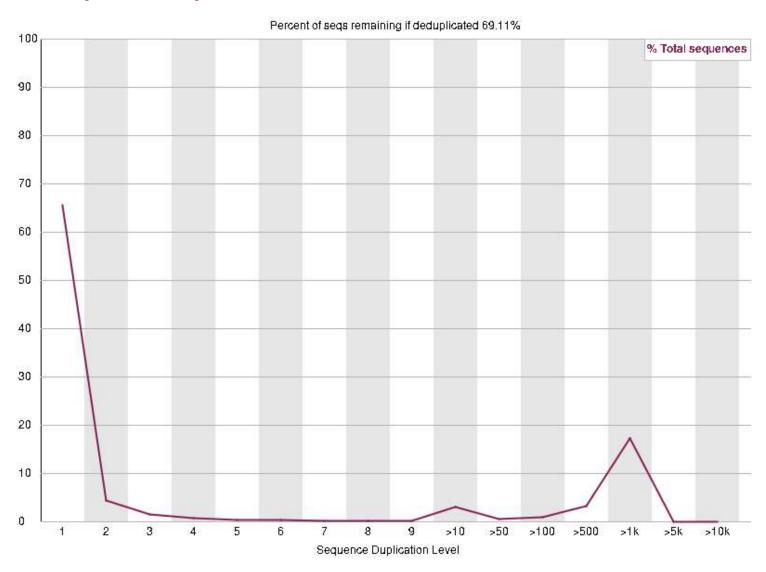
Per base N content



Sequence Length Distribution



Sequence Duplication Levels



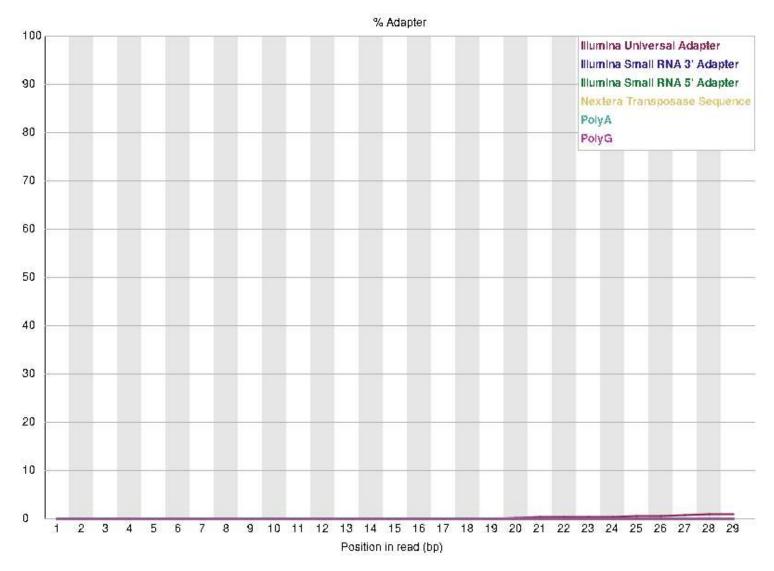
Overrepresented sequences

Sequence	Count	Percentage	Possible Source
AGAGTTTTATCGCTTCCATGACGCAGAAGTTAACACTTTC	2065	0.5224039181558763	No Hit
GATTGGCGTATCCAACCTGCAGAGTTTTATCGCTTCCATG	2047	0.5178502762542754	No Hit
ATTGGCGTATCCAACCTGCAGAGTTTTATCGCTTCCATGA	2014	0.5095019327680071	No Hit
CGATAAAAATGATTGGCGTATCCAACCTGCAGAGTTTTAT	1913	0.4839509420979134	No Hit
GTATCCAACCTGCAGAGTTTTATCGCTTCCATGACGCAGA	1879	0.47534961850600066	No Hit
AAAAATGATTGGCGTATCCAACCTGCAGAGTTTTATCGCT	1846	0.4670012750197325	No Hit
TGATTGGCGTATCCAACCTGCAGAGTTTTATCGCTTCCAT	1841	0.46573637449150995	No Hit

Sequence	Count	Percentage	Possible Source
AACCTGCAGAGTTTTATCGCTTCCATGACGCAGAAGTTAA	1836	0.46447147396328753	No Hit
GATAAAAATGATTGGCGTATCCAACCTGCAGAGTTTTATC	1831	0.4632065734350651	No Hit
ATGATTGGCGTATCCAACCTGCAGAGTTTTATCGCTTCCA	1779	0.45005160794155147	No Hit
AAATGATTGGCGTATCCAACCTGCAGAGTTTTATCGCTTC	1779	0.45005160794155147	No Hit
AATGATTGGCGTATCCAACCTGCAGAGTTTTATCGCTTCC	1760	0.4452449859343061	No Hit
AAAATGATTGGCGTATCCAACCTGCAGAGTTTTATCGCTT	1729	0.4374026026593269	No Hit
CGTATCCAACCTGCAGAGTTTTATCGCTTCCATGACGCAG	1713	0.43335492096901496	No Hit
ATCCAACCTGCAGAGTTTTATCGCTTCCATGACGCAGAAG	1708	0.43209002044079253	No Hit
CAGAGTTTTATCGCTTCCATGACGCAGAAGTTAACACTTT	1684	0.42601849790532476	No Hit
TGCAGAGTTTTATCGCTTCCATGACGCAGAAGTTAACACT	1668	0.4219708162150128	No Hit
CAACCTGCAGAGTTTTATCGCTTCCATGACGCAGAAGTTA	1668	0.4219708162150128	No Hit
TATCCAACCTGCAGAGTTTTATCGCTTCCATGACGCAGAA	1630	0.4123575722005221	No Hit
GTCATGGAAGCGATAAAACTCTGCAGGTTGGATACGCCAA	1620	0.40982777114407726	No Hit
AACTTCTGCGTCATGGAAGCGATAAAACTCTGCAGGTTGG	1616	0.4088158507214993	No Hit
GCAGAGTTTTATCGCTTCCATGACGCAGAAGTTAACACTT	1580	0.39970856691829754	No Hit
TGGCGTATCCAACCTGCAGAGTTTTATCGCTTCCATGACG	1569	0.3969257857562082	No Hit
GGCGTATCCAACCTGCAGAGTTTTATCGCTTCCATGACGC	1542	0.39009532290380683	No Hit
ATAAAAATGATTGGCGTATCCAACCTGCAGAGTTTTATCG	1481	0.37466353645949285	No Hit
ACCTGCAGAGTTTTATCGCTTCCATGACGCAGAAGTTAAC	1479	0.37415757624820384	No Hit
ATGGAAGCGATAAAACTCTGCAGGTTGGATACGCCAATCA	1452	0.3673271133958026	No Hit
GATAAAACTCTGCAGGTTGGATACGCCAATCATTTTTATC	1420	0.35923175001517876	No Hit
CGTCATGGAAGCGATAAAACTCTGCAGGTTGGATACGCCA	1412	0.3572079091700229	No Hit
ACTTCTGCGTCATGGAAGCGATAAAACTCTGCAGGTTGGA	1368	0.34607678452166524	No Hit
TAACTTCTGCGTCATGGAAGCGATAAAACTCTGCAGGTTG	1363	0.34481188399344276	No Hit
CATGGAAGCGATAAAACTCTGCAGGTTGGATACGCCAATC	1333	0.337222480824108	No Hit
CGATAAAACTCTGCAGGTTGGATACGCCAATCATTTTTAT	1304	0.32988605776041774	No Hit
TAAAAATGATTGGCGTATCCAACCTGCAGAGTTTTATCGC	1277	0.32305559490801644	No Hit
GCGTATCCAACCTGCAGAGTTTTATCGCTTCCATGACGCA	1262	0.31926089332334906	No Hit
TGCGTCATGGAAGCGATAAAACTCTGCAGGTTGGATACGC	1233	0.3119244702596588	No Hit
GGAAGCGATAAAACTCTGCAGGTTGGATACGCCAATCATT	1182	0.2990224848717897	No Hit
AAGCGATAAAACTCTGCAGGTTGGATACGCCAATCATTTT	11 36	0.2873854000121431	No Hit
ACTCTGCAGGTTGGATACGCCAATCATTTTTATCGAAGCG	1133	0.28662645969520956	No Hit
AAACTCTGCAGGTTGGATACGCCAATCATTTTTATCGAAG	1131	0.2861204994839206	No Hit
AAAACTCTGCAGGTTGGATACGCCAATCATTTTTATCGAA	1129	0.2856145392726316	No Hit
AGCGATAAAACTCTGCAGGTTGGATACGCCAATCATTTTT	1113	0.2815668575823197	No Hit
ATAAAACTCTGCAGGTTGGATACGCCAATCATTTTTATCG	1111	0.28106089737103074	No Hit

Sequence	Count	Percentage	Possible Source
${\tt AACTCTGCAGGTTGGATACGCCAATCATTTTTATCGAAGC}$	1083	0.273977454412985	No Hit
${\tt CTGCAGAGTTTTATCGCTTCCATGACGCAGAAGTTAACAC}$	1055	0.2668940114549392	No Hit
TTCTGCGTCATGGAAGCGATAAAACTCTGCAGGTTGGATA	947	0.23957216004533402	No Hit
TGGAAGCGATAAAACTCTGCAGGTTGGATACGCCAATCAT	946	0.23931917993968954	No Hit
TAAAACTCTGCAGGTTGGATACGCCAATCATTTTTATCGA	912	0.2307178563477768	No Hit
GAAGCGATAAAACTCTGCAGGTTGGATACGCCAATCATTT	888	0.224646333812309	No Hit
GCGTCATGGAAGCGATAAAACTCTGCAGGTTGGATACGCC	805	0.20364898504381615	No Hit
GCGATAAAACTCTGCAGGTTGGATACGCCAATCATTTTTA	785	0.19858938293092632	No Hit
TTGGCGTATCCAACCTGCAGAGTTTTATCGCTTCCATGAC	784	0.1983364028252818	No Hit
${\tt CTTCTGCGTCATGGAAGCGATAAAACTCTGCAGGTTGGAT}$	762	0.192770840501103	No Hit
${\tt TCCAACCTGCAGAGTTTTATCGCTTCCATGACGCAGAAGT}$	752	0.19024103944465806	No Hit
${\tt CCAACCTGCAGAGTTTTATCGCTTCCATGACGCAGAAGTT}$	744	0.18821719859950212	No Hit
TCATGGAAGCGATAAAACTCTGCAGGTTGGATACGCCAAT	665	0.16823177025358726	No Hit
${\tt TCTGCGTCATGGAAGCGATAAAACTCTGCAGGTTGGATAC}$	627	0.15861852623909656	No Hit
CCTGCAGAGTTTTATCGCTTCCATGACGCAGAAGTTAACA	613	0.15507680476007366	No Hit
CGGTTCAGCAGGAATGCCGAGATCGGAAGAGCGGTTCAGC	599	0.15153508328105078	Illumina Paired End PCR Primer 2 (96% over 25bp)
TCTGCAGGTTGGATACGCCAATCATTTTTATCGAAGCGCG	585	0.1479933618020279	No Hit
CGCTTAAAGCTACCAGTTATATGGCTGGGGGGTTTTTTTT	552	0.13964501831575965	No Hit
${\tt CTCTGCAGGTTGGATACGCCAATCATTTTTATCGAAGCGC}$	532	0.1345854162028698	No Hit
${\tt CTGCGTCATGGAAGCGATAAAACTCTGCAGGTTGGATACG}$	515	0.13028475440691342	No Hit
${\tt CTGCAGGTTGGATACGCCAATCATTTTTATCGAAGCGCGC}$	505	0.12775495335046852	No Hit
GCTTAAAGCTACCAGTTATATGGCTGGGGGGTTTTTTTTG	411	0.10397482341988626	No Hit

Adapter Content



Produced by FastQC (version 0.12.1)